

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:17:08 ; Search time 10 Seconds

Sequence: 1 LYVYDCTESQNLICLEGSN.....PKPQSHNDGDFEEIPEEYLQ 65
 (without alignments)
 112.542 Million cell. updates/sec

Title: US-09-664-326-23

Perfect score: 368
 Sequence: 1 LYVYDCTESQNLICLEGSN.....PKPQSHNDGDFEEIPEEYLQ 65

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 109717 seqs, 17314136 residues

Total number of hits satisfying chosen parameters: 109717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pupbaa/us08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pupbaa/pct_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pupbaa/us06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pupbaa/us06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pupbaa/us07_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pupbaa/us07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pupbaa/pctus_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pupbaa/us08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pupbaa/us09_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pupbaa/us09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pupbaa/us10_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pupbaa/us10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pupbaa/us60_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pupbaa/us60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368	100.0	65	9	US-09-899-235-15
2	113.5	30.8	73	10	Sequence 15, Appl
3	77	20.9	14	10	Sequence 12, Appl
4	77	20.9	14	10	Sequence 21, Appl
5	77	20.9	15	10	Sequence 25, Appl
6	77	20.9	15	10	Sequence 18, Appl
7	70	19.0	160	10	Sequence 10, Appl
8	70	19.0	323	10	Sequence 9, Appl
9	70	19.0	658	10	Sequence 85, Appl
10	70	19.0	658	10	Sequence 83, Appl
11	70	18.8	315	9	Sequence 65, Appl
12	69	18.8	1218	10	Sequence 7, Appl
13	68.5	18.6	1218	10	Sequence 34, Appl
14	66.5	18.1	810	10	Sequence 6, Appl
15	66	17.9	197	12	Sequence 12, Appl
16	64	17.4	18	10	Sequence 5, Appl
17	64	17.4	51	12	Sequence 43222, A
18	64	17.4	379	10	Sequence 7, Appl
19	63.5	17.3	568	10	US-09-945-676-7

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

ALIGNMENTS

RESULT 1
 US-09-899-235-15
 ; Sequence 15, Application US/09899235
 ; Patent No. US2002177620A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HABERMANN, PAUL
 ; TITLE OF INVENTION: BIFUNCTIONAL FUSION PROTEINS FORMED FROM HIRUDIN AND
 ; TITLE OF INVENTION: TAP
 ; FILE REFERENCE: 024B1.1750-00
 ; CURRENT APPLICATION NUMBER: US/09/899, 235
 ; CURRENT FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 65
 ; FEATURE:
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Amino acid
 ; OTHER INFORMATION: sequence of Refudan (Leu - hirudin)
 ; US-09-899-235-15

Query Match 100.0%; Score 368; DB 9; Length 65;

Best Local Similarity 100.0%; Pred. No. 9, 6e-33;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYVYDCTESQNLICLEGSN.....PKPQSHNDGDFEEIPEEYLQ 65
 Db 1 LYVYDCTESQNLICLEGSN.....PKPQSHNDGDFEEIPEEYLQ 60

QY 61 EEEYLQ 65
 Db 61 EEEYLQ 65

RESULT 2
 US-09-779-054-12
 ; Sequence 12, Application US/09779054
 ; Patent No. US2002120102A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lu, Xinjie
 ; APPLICANT: Kakkar, Vijay

RESULTS

RESULT 4

US-09-925-715-25

; Sequence 25, Application US/09925715

; Patent No. US20020102217A1

; GENERAL INFORMATION:

; APPLICANT: Nycomed Imaging AS

; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic FILE REFERENCE: REF/Klaveness/206

CURRENT APPLICATION NUMBER: US/09/925,715

CURRENT FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 25

LENGTH: 14

FEATURE: OTHER INFORMATION: Modified dendroaspin (KGDM-dendroaspin-Hc)

US-09-779-054-12

Query Match 30.8%; Score 113.5; DB 10; Length 73;

Best Local Similarity 64.7%; Pred. No. 9.5e-06;

Matches 22; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

Qy 39 CIVGSEI-----PKPQSHNDGDFEEIPPEYIQL 65

Db 40 CFPKQDMPGPYCPRPQSHNDGDFEEIPPEYIQL 73

RESULT 3

US-09-765-614B-29

; Sequence 29, Application US/09765614B

; Patent No. US20020102215A1

; GENERAL INFORMATION:

; APPLICANT: Nycomed Imaging AS

; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic FILE REFERENCE: REF/Klaveness/054

CURRENT APPLICATION NUMBER: US/09/765,614B

CURRENT FILING DATE: 2001-07-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn ver. 2.1

SEQ ID NO: 29

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial

OTHER INFORMATION: Sequence:Thrombus

OTHER INFORMATION: binding peptide

US-09-765-614B-29

Query Match 20.9%; Score 77; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 NDGDFEEIPPEYIQL 65

Db 1 NDGDFEEIPPEYIQL 14

RESULT 4

US-09-925-715-25

; Sequence 25, Application US/09925715

; Patent No. US20020102217A1

; GENERAL INFORMATION:

; APPLICANT: Nycomed Imaging AS

; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic FILE REFERENCE: REF/Klaveness/206

CURRENT APPLICATION NUMBER: US/09/925,715

CURRENT FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 25

LENGTH: 14

FEATURE: OTHER INFORMATION: Description of Artificial Sequence

US-09-925-715-25

Query Match 20.9%; Score 77; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 NDGDFEEIPPEYIQL 65

Db 1 NDGDFEEIPPEYIQL 14

RESULT 5

US-09-765-614B-18

; Sequence 18, Application US/09765614B

; Patent No. US20020102215A1

; GENERAL INFORMATION:

; APPLICANT: Nycomed Imaging AS

; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic FILE REFERENCE: REF/Klaveness/054

CURRENT APPLICATION NUMBER: US/09/765,614B

CURRENT FILING DATE: 2001-07-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 18

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial

OTHER INFORMATION: Sequence:Lipopeptide

NAME/KEY: MOD_RBS

LOCATION: (1)

OTHER INFORMATION: Dipalmitoyl-Lys

NAME/KEY: MOD_RBS

LOCATION: (15)

OTHER INFORMATION: AMIDATION

US-09-765-614B-18

Query Match 20.9%; Score 77; DB 10; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 NDGDFEEIPPEYIQL 65

Db 2 NDGDFEEIPPEYIQL 15

RESULT 6

US-09-925-715-18

; Sequence 18, Application US/09925715

; Patent No. US20020102217A1

; GENERAL INFORMATION:

; APPLICANT: Nycomed Imaging AS

; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic FILE REFERENCE: REF/Klaveness/206

CURRENT APPLICATION NUMBER: US/09/925,715

CURRENT FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 18

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: Lipopeptide with an affinity for thrombin

NAME/KEY: MOD_RES

LOCATION: (1)

OTHER INFORMATION: dipalmitoyl-lysine

LOCATION: (15)

OTHER INFORMATION: amidation

US-09-925-715-18

RESULT 7

Query Match 20.9%; Score 77; DB 10; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 NDGDFEEIPEEYLQ 65

||||||||| 15

Db 2 NDGDFEEIPEEYLQ 15

RESULT 7

US-09-798-042-100

Sequence 100, Application US/09798042

PATENT NO. US20020068343A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS OF INVENTION: AND TREATMENT OF EHRlichIA INFECTION

FILE REFERENCE: 210121.439C7

CURRENT APPLICATION NUMBER: US/09798, 042

CURRENT FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 108

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 100

LENGTH: 160

TYPE: PRT

ORGANISM: Ehrlichia sp.

US-09-798-042-100

Query Match 19.0%; Score 70; DB 10; Length 160;

Best Local Similarity 29.6%; Pred. No. 0.88;

Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

QY 6 CTESGQNCLCCEGSNVCGQGN----KCILGSDGKRN-QCVTGEGSTPKPQSHNDGDP-- 56

Db 79 CGDNGSSITTSGTNTSETGQVFRDFIRATLKEKGSKNWPSSGTTPKPVNDNAKAVA 138

QY 57 -----EEIPEE 62

Db 139 KDLVQELTPPE 149

RESULT 8

US-09-159-469-9

Sequence 9, Application US/09159469

PATENT NO. US2002006453A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS OF INVENTION: AND TREATMENT OF EHRlichIA INFECTION

FILE REFERENCE: 210121.439C7

CURRENT APPLICATION NUMBER: US/09798, 042

CURRENT FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 108

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 9

LENGTH: 323

TYPE: PRT

ORGANISM: Ehrlichia sp.

US-09-159-469-9

Query Match 19.0%; Score 70; DB 10; Length 323;

Best Local Similarity 29.6%; Pred. No. 1.9;

Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

QY 6 CTESGQNCLCCEGSNVCGQGN----KCILGSDGKRN-QCVTGEGSTPKPQSHNDGDP-- 56

Db 185 CGDNGSSITTSGTNTSETGQVFRDFIRATLKEKGSKNWPSSGTTPKPVNDNAKAVA 244

QY 57 -----EEIPEE 62

Db 245 KDLVQELTPPE 255

RESULT 9

US-09-798-042-9

Sequence 9, Application US/09798042

PATENT NO. US20020068343A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS OF INVENTION: AND TREATMENT OF EHRlichIA INFECTION

FILE REFERENCE: 210121.439C7

CURRENT APPLICATION NUMBER: US/09798, 042

CURRENT FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 108

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 9

LENGTH: 323

TYPE: PRT

ORGANISM: Ehrlichia sp.

US-09-159-469-9

Query Match 19.0%; Score 70; DB 10; Length 323;

Best Local Similarity 29.6%; Pred. No. 1.9;

Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

QY 6 CTESGQNCLCCEGSNVCGQGN----KCILGSDGKRN-QCVTGEGSTPKPQSHNDGDP-- 56

Db 185 CGDNGSSITTSGTNTSETGQVFRDFIRATLKEKGSKNWPSSGTTPKPVNDNAKAVA 244

QY 57 -----EEIPEE 62

Db 245 KDLVQELTPPE 255

RESULT 10
 US-09-798-042-85
 ; Sequence 85, Application US/09798042
 ; Patent No. US20020068343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; Lodes, Michael J.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 ; FILE REFERENCE: 210121.439C7
 ; CURRENT APPLICATION NUMBER: US/09/798, 042
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 85
 ; LENGTH: 658
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Amino acid sequence of fusion protein containing
 ; OTHER INFORMATION: HGP-3 and HGP-1 antigens
 ; US-09-798-042-85

Query Match 19.0%; Score 70; DB 10; Length 658;
 Best Local Similarity 29.6%; Pred. No. 3.9; Mismatches 10; Indels 14; Gaps 3;
 Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

QY 6 CTESQNLCLCSEGNSVCGQDN-----KCILGSDEKN-QCVTGEGTPKQPSHQHNGDF~ 56
 Db 194 CGDNGSSTTTSGTANVSETGQVFRDPIRATLKEGDSKNWPSSGTTGTPKPVNDNAKAVA 253

QY 57 --- EEEPEE 62
 Db 254 KDLVQBLTPEE 264

RESULT 11
 US-09-798-042-93
 Sequence 93, Application US/09798042
 ; Patent No. US20020068343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 ; FILE REFERENCE: 210121.439C7
 ; CURRENT APPLICATION NUMBER: US/09/798, 042
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 93
 ; LENGTH: 658
 ; TYPE: PRT
 ; ORGANISM: Ehrlichia

Query Match 19.0%; Score 70; DB 10; Length 658;
 Best Local Similarity 29.6%; Pred. No. 3.9; Mismatches 10; Indels 14; Gaps 3;
 Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

QY 6 CTESQNLCLCSEGNSVCGQDN-----KCILGSDEKN-QCVTGEGTPKQPSHQHNGDF~ 56
 Db 194 CGDNGSSTTTSGTANVSETGQVFRDPIRATLKEGDSKNWPSSGTTGTPKPVNDNAKAVA 253

QY 57 --- EEEPEE 62
 Db 254 KDLVQBLTPEE 264

RESULT 12
 US-09-808-602-65
 ; Sequence 65, Application US/09808602
 ; Patent No. US2002015515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Verne, Corine A
 ; APPLICANT: Fernandes, Elma
 ; APPLICANT: Shimelis, Richard A
 ; APPLICANT: Herrman, John L
 ; APPLICANT: Majundar, Kumud
 ; APPLICANT: Mishra, Vishnu
 ; APPLICANT: MacDougall, John
 ; TITLE OF INVENTION: No. US2002015515A1el Proteins and Nucleic Acids Encoding Same
 ; CURRENT APPLICATION NUMBER: US/09/808, 602
 ; FILE REFERENCE: 15966-697.CIP
 ; CURRENT FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 09/800, 198
 ; PRIOR FILING DATE: 2001-03-05
 ; PRIOR APPLICATION NUMBER: 60/186, 596
 ; PRIOR FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 65
 ; LENGTH: 315
 ; TYPE: PRT
 ; ORGANISM: Gallus gallus
 US-09-808-602-65

Query Match 18.8%; Score 69; DB 9; Length 315;
 Best Local Similarity 33.3%; Pred. No. 2.3; Mismatches 6; Indels 10; Gaps 3;
 Matches 21; Conservative 6; Mismatches 26; Indels 10; Gaps 3;

QY 7 TESGONLCLC-----EGSNVCGQGNKNCIG-SDEGEKNQCVTGEGTPKQPSHQHNGDFERI 59
 Db 45 TEKGSPTCLCIEQCKPHGRVCGSGNKTYLINHCELHRDACLITGS--KIQVVDGHCKEK 101

QY 60 PEE 62
 Db 102 KSE 104

RESULT 13
 US-09-855-722-7
 ; Sequence 7, Application US/09855722
 ; Patent No. US20020049306A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sakano, Seiji
 ; APPLICANT: Itoh, Akira
 ; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
 ; FILE REFERENCE: KP-8576
 ; CURRENT APPLICATION NUMBER: US/09/855, 722
 ; CURRENT FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: 09/214, 278
 ; PRIOR FILING DATE: 1999-01-26
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 7
 ; LENGTH: 1218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-855-722-7

Query Match 18.6%; Score 68.5%; DB 10; Length 1218;
 Best Local Similarity 28.6%; Pred. No. 11; Mismatches 5; Indels 29; Gaps 4;
 Matches 23; Conservative 5; Mismatches 23; Indels 29; Gaps 4;

QY 6 CTESQNLCLCSEGNSVCGQDN-----KCILGSDEKN-QCVTGEGTPKQPSHQHNGDF~ 56
 Db 276 CNEPQQ---CLCETNWGGQQLDKDQINCYCQHQPCLNGGTCSTGPDKYOCPECIGSNS 333

QY 57 --- EEEPEE 62
 Db 276 CNEPQQ---CLCETNWGGQQLDKDQINCYCQHQPCLNGGTCSTGPDKYOCPECIGSNS 333

RESULT 14
 US-09-976-165-34
 ; Sequence 34, Application US/09976165
 ; Patent No. US20020107383A1
 GENERAL INFORMATION:
 APPLICANT: FUJIWARA, TSUTOMU
 APPLICANT: WATANABE, TAKESHI
 APPLICANT: HORIE, MASATO
 TITLE OF INVENTION: AN ISOLATED NUCLEAR ACID MOLECULE ENCODING HUMAN
 SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
 FILE REFERENCE: Q-53599
 CURRENT APPLICATION NUMBER: US/09/976,165
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/565,538
 PRIOR FILING DATE: 2000-05-05
 PRIOR APPLICATION NUMBER: 09/055,699
 PRIOR FILING DATE: 1998-04-07
 PRIOR APPLICATION NUMBER: 08/820,170
 PRIOR FILING DATE: 1997-03-19
 PRIOR APPLICATION NUMBER: JP 63410/1996
 PRIOR FILING DATE: 1996-03-19
 PRIOR APPLICATION NUMBER: JP 69163/1997
 PRIOR FILING DATE: 1997-03-05
 NUMBER OF SEQ ID NOS: 95
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 34
 LENGTH: 810
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 15
 US-10-040-916-6
 ; Sequence 6, Application US/10040916
 ; Patent No. US2002014676A1
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth
 McCoy, John
 Lavallie, Edward
 Racine, Lisa
 Merberg, David
 Treacy, Maurice
 Evans, Cheryl
 Spaulding, Vicki
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

Qy 1 LNYTDTESQNLICLEGSNVCGQGNKICLGSDEKKN-----QCVTGEGTPPK 4
 Db 38 VNSTGTTEDGEGPASCTGSEXCXEG--FAISSEEEENGESAMDSTVAKEGTNVP 8

Qy 1 LNYTDTESQNLICLEGSNVCGQGNKICLGSDEKKN-----QCVTGEGTPPK 4
 Db 38 VNSTGTTEDGEGPASCTGSEXCXEG--FAISSEEEENGESAMDSTVAKEGTNVP 8

Search completed: December 30, 2002, 16:21:06
 Job time : 10 secs

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/040,916
 FILING DATE: 07-Jan-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/887,029
 FILING DATE: 07-FEB-1997
 APPLICATION NUMBER: 08/686,878
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8224
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 MOLECULE TYPE: protein
 SUBSEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-10-040-916-6

